Journal of Microbiology and Biotechnology 2014 vol.24 N11, pages 1464-1472

Microbial community diversity in anaerobic reactors digesting turkey, chicken, and swine wastes

Ziganshina E., Belostotskiy D., Shushlyaev R., Miluykov V., Vankov P., Ziganshin A.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

© 2014 by The Korean Society for Microbiology and Biotechnology. The microbial community structures of two continuous stirred tank reactors digesting turkey manure with pine wood shavings as well as chicken and swine manure were investigated. The reactor fed with chicken/swine wastes displayed the highest organic acids concentration (up to 15.2 g/l) and ammonia concentration (up to 3.7 g/l ammonium nitrogen) and generated a higher biogas yield (up to 366 ml/gVS) compared with the reactor supplied with turkey wastes (1.5– 1.8 g/l of organic acids and 1.6–1.7 g/l of ammonium levels; biogas yield was up to 195 ml/gVS). The microbial community diversity was assessed using both sequencing and profiling terminal restriction fragment length polymorphisms of 16S rRNA genes. Additionally, methanogens were analyzed using methyl coenzyme M reductase alpha subunit (mcrA) genes. The bacterial community was dominated by members of unclassified Clostridiales with the prevalence of specific clostridial phylotypes in each reactor, indicating the effect of the substrate type on the community structure. Of the methanogenic archaea, methanogens of the genus Methanosarcina were found in high proportions in both reactors with specific methanosarcinas in each reactor, whereas the strict hydrogenotrophic methanogens of Methanoculleus sp. were found at significant levels only in the reactor fed with chicken/swine manure (based on the analyses of 16S rRNA gene). This suggests that among methanogenic archaea, Methanosarcina species which have different metabolic capabilities, including aceticlastic and hydrogenotrophic methanogenesis, were mainly involved in anaerobic digestion of turkey wastes.

http://dx.doi.org/10.4014/jmb.1404.04043

Keywords

16S rRNA genes, Agricultural wastes, Anaerobic digestion, McrA genes